Supplementary Material 1

A. Biases control of the home range size variable included in the analysis of the variation in annual reproductive success of Siberian chipmunks *Tamias* (*Eutamias*) *sibiricus barberi* introduced in the Forêt de Sénart (France).

A.1. Periphery index

Best-ranked models with change in Δ_{QAICc} examining the variation of the periphery index according to habitat and sex using a generalized linear model with quasibinomial errors and logit link (Dispersion parameter for quasibinomial family taken to be 5.06). Selected model in bold.

Candidate models	*K*	QAICc	Δ_{QAICc}	*w*
Sex	**2**	**561.13**	**0.00**	**0.49**
Habitat + Sex	3	561.65	0.52	0.38
Habitat + Sex + Habitat:Sex	4	563.64	2.51	0.14

The periphery index varied according to sex, averaged model coefficients (a.m.c.) being 0.57 ± 0.14 ($P < 0.01$) for males. No effect of habitat was detected (a.m.c.: 0.18 ± 0.15, $P = 0.24$, for the open habitat). The residuals of the fit including sex as independent variable was used as a periphery index (PI) in the following analyses.

A.2. Number of captures

Best-ranked models with change in $\Delta_{AICc} < 4.0$ examining the variation of the log(+1) transformed number of captures according to habitat, sex and periphery index using a linear model. Selected model in bold.

Candidate models	*K*	AICc	Δ_{AICc}	*w*
Periphery index	**3**	**207.75**	**0.00**	**0.40**
Habitat + Periphery index + Habitat:Periphery index	5	209.18	1.44	0.19
Habitat + Periphery index	4	209.80	2.05	0.14
Periphery index + Sex	4	209.93	2.18	0.13
Null model	2	211.25	3.50	0.07
Habitat + Periphery index + Habitat:Periphery index + Sex	6	211.42	3.67	0.06

The number of captures decreased as the periphery index increased (a.m.c.: -0.12 ± 0.05, P = 0.03), without any relationships with habitat (a.m.c.: 0.16 ± 0.09, P = 0.10, for the open habitat) or sex (a.m.c.: 0.05 ± 0.21, P = 0.80, for males). The residuals of the fit including periphery index as independent variable was used as a capture number index (CNI) in the following analyses.

A.3. Home range size

Best-ranked models with change in Δ_{AICc} examining the variation of the home range size based on 5 data points (n = 64), Log(+1) transformed, according to habitat and sex, including periphery and capture number indices, using a linear model using a simple linear model. Selected model in bold.

Candidate models	*K*	AICc	Δ_{AICc}	*w*
HAB + SEX + HAB:SEX + PI + CNI	**7**	**4.27**	**0.00**	**0.71**
HAB + SEX + PI + CNI	6	6.09	1.82	0.29

As expected, home range size was negatively related to the periphery index (a.m.c.: -0.04 ± 0.01, P < 0.01), indicating that home range sizes were smallest at the edge of the trapping grid. Moreover, home range size was dependent upon the number of captures of chipmunks (a.m.c.: 0.16 ± 0.04, P < 0.01), indicating that the more a chipmunk was trapped, the greatest was its home range. Finally, home range size varied according to sex and habitat (a.m.c.: 0.25 ± 0.13, P = 0.05). Home range size index corresponded to the residuals calculated from the fit given by the selected model, which was included as a covariate in the analysis of the variation in annual reproductive success.

B. R-code for the 'Delete-one' Jackknife procedure used to calculate the directionnal selection gradient

```
##Loop for running a 'delete-one' simple linear regression
jackkslr <- list(n)
for (i in 1:n) {
jackkslr [[i]] <- lm(fitness ~ trait, data = data[-i, ])
 }
##Store coefficients of the i^th linear regressions
coeff.matrix <- matrix(0, nrow = n, ncol = 2)
for (i in 1: n) {
coeff.matrix[i, ] <- coef(jackkslr[[i]])
 }
colnames(coeff.matrix) <- c("INTERCEPT", "COEFF")
##Create a table of the i coefficients
seltab=data.frame(round(coeff.matrix, 2))
print(seltab)
##Calculate the averaged coefficient, corresponding to the selection gradient and its standard deviation
mean(seltab$COEFF)
sd(seltab$COEFF)
```

Supplementary material 2

Forward (F) and reverse (R) primers for amplification of microsatellites in *Tamias sibiricus*. Also listed are the total number of alleles and the observed heterozygosity (H_o) at each locus. Locus whose primers were redesigned for *T. sibiricus* are indicated by the suffix 'sib'

Locus name	Sequences 5′–3′		N. of alleles	H_o
[(1)] EuAm94	F	TGGCTCAGTTTTTCAGTTTTT	8	0.33
	R	ATCTCAAAGCCATCAAGAGTTT		
[(1)] EuAm41	F	ATTCAGGCTCCAGAAAAACAAA	5	0.36
	R	TCTGCCCCAGAGATATTGATCT		
[(1)] EuAm35	F	ATCCGTTTAGTCTGTTATGTCTCA	7	0.79
	R	TTTAATCTAAAGGACAACAATTGC		
[(1)] EuAm108sib	F	GTCTCTAACAATTTGAACAA	5	0.71
	R	CATGTTTGGGMGTGGTCATG		
[(1)] EuAm138	F	AATGTATGCTAGAGTGCCCAC	6	0.74
	R	TTTTCTAGAGACACAAAAATTTAG		
[(2)] Chip14sib	F	TCAAGAAATACTTGGTAAGATGGAG	4	0.51
	R	TTGTTTACGAGATCTTCATTTCAG		
[(2)] Chip31sib	F	ATGGAACAACAGCCTACCAG	5	0.59
	R	TTTAAACCCCTTACCCTCTTTG		
[(2)] Chip32sib	F	TGTCCTAAACTTAGGTAGTTT	4	0.05
	R	CTCAGTAACTTAGCAAGACC		
[(2)] Chip205sib	F	TGTGCCTAGAGTCAGTGAATGG	6	0.54
	R	CACATTTCCAGTTTTCTTTGGAG		

[(1)] Peters MB, Glenn JL, Svete P, Hagen C, Tsyusko OV, Decoursey P, Lieutenant-Gosselin M, Garant D, Glenn T 2007 Development and characterization of microsatellite loci in the eastern chipmunk *Tamias striatus*. Molecular Ecology Notes 7:877–879

[(2)] Schulte-Hostedde AI, Gibbs HL, Millar JS 2000 Microsatellite DNA loci suitable for parentage analysis in the Yellow-pine chipmunk *Tamias amoenus*. Molecular Ecology 9:2180–2181